

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2001, 18:13:54 ; Search time 30.78 Seconds
(without alignments)
1591.301 Million cell updates/sec

Title: US-09-405-504A-53
Perfect score: 3384
Sequence: 1 MLLGASLVGLLFSKLVKL.....RYVPLDQAYSRIOAGEEKL 643

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2110	62.4	646	1 A55093	fatty acid transpo
2	1292	38.2	650	2 T21498	hypothetical prote
3	1281	37.9	655	2 T15879	hypothetical prote
4	974	28.8	689	1 JN0107	very-long-chain ac
5	918.5	27.1	608	2 H83284	probable very-long
6	886.5	26.2	597	2 D70609	probable fadD6 pr
7	801	23.7	643	2 T43052	fatty acid transpo
8	714	21.1	623	2 S45899	probable membrane
9	408	12.1	502	2 D70806	probable fadD17 pr
10	389	11.5	503	2 E70853	probable acid--CoA
11	375	11.1	569	2 C69471	probable fatty-aci
12	369.5	10.9	522	2 H85484	probable crotonobe
13	364.5	10.8	513	2 A69831	probable acid--CoA
14	358	10.6	532	2 G70986	probable coA ligas
15	350.5	10.4	522	2 S40558	probable carnitine
16	332	9.8	599	2 H72454	probable fatty-aci
17	322.5	9.5	560	2 A70628	probable acid--CoA
18	312.5	9.2	561	2 F85791	hypothetical prote
19	311.5	9.2	549	2 F69893	probable acid--CoA
20	311.5	9.2	561	1 S41589	long-chain-fatty-a
21	310	9.2	2723	2 T03221	probable polyketid
22	303	9.0	545	1 A39827	4-coumarate--CoA
23	301.5	8.9	485	2 H69556	0-succinylbenzoate
24	300.5	8.9	549	2 T44812	probable fatty-aci
25	300	8.9	545	1 B39827	4-coumarate--CoA
26	298.5	8.8	593	2 E69378	probable acid--CoA
27	294.5	8.7	552	2 E69438	probable fatty-aci
28	294	8.7	554	2 A70904	probable acid--CoA
29	293.5	8.7	512	2 T41164	coenzyme a synthet

30 293.5 8.7 561 2 D96674 hypothetical prote
31 292 8.6 584 2 C75364 probable long-chain
32 291 8.6 444 2 T50931 hypothetical prote
33 291 8.6 535 2 T08074 4-coumarate--CoA
34 286 8.5 544 1 S01667 polyketide synthas
35 286 8.5 8563 2 T30226 probable acid--CoA
36 285.5 8.4 517 2 D81101 4-coumarate--CoA
37 285 8.4 548 2 T07908 probable acid--CoA
38 284 8.4 535 2 F70914 4-coumarate--CoA
39 283.5 8.4 517 2 D81839 probable acid--CoA
40 282 8.3 544 2 S15695 probable acyl-CoA
41 282 8.3 555 2 A83327 4-coumarate--CoA
42 280.5 8.3 541 2 T34850 probable AMP-bind
43 280.5 8.3 570 2 T08075 probable acid--CoA
44 280 8.3 645 2 A83054 4-coumarate--CoA
45 277 8.2 549 2 G69335 acetyl-coenzyme A
probable acid--CoA

ALIGNMENTS

RESULT 1

A55093

fatty acid transport protein precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Sep-2000

C:Accession: A55093; I49132

R:Schafer, J.E.; Lodish, H.F.

Cell 79, 427-436, 1994

A:Title: Expression cloning and characterization of a novel adipocyte long chain fatty acid

A:Reference number: A55093; MUID:95042740

A:Accession: A55093

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-646 <SCH>

A:Cross-references: GB:U15976; NID:G563828; PIDN:AAC71060.1; PID:G563829

C:Genetics:

A:Gene: FATP

C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase

F:124-604/Domain: acetate--CoA ligase homology <ACL>

Query Match	62.4%	Score	2110;	DB	1;	Length	646;
Best Local Similarity	60.9%;	Pred. No.	1.1e-164;				
Matches	391;	Conservative	97;	Mismatches	152;	Indels	2;
Gaps	2;						
QY	4	GASLVGLLFSKL-VLKLPWTQVGSLLFLYLGSGGWRFFIRVFIKTRDIFGGLVLLKV	62				
Db	5	GAGTASVASLALLWFLGLPWTWSAAAAAFVYVGGGWRFLRIVCKTARRDLFGSLVLRV	64				
QY	63	KAKVRCLOERRVPILFASVTRRHDPKTLIFEGTDTHTWTFPQLDEYSSSVANFLQARG	122				
Db	65	RLRLRRHRRAGDTIPCFIQFQAVRRQERLALVDVASSGICWTFQAQLDYSNAVANFLRQLG	124				
QY	123	LASGDVAALFMENRNFVGLWGLMAKLYEAAALINTLRDALLHCLTTSRAALVFGSE	182				
Db	125	FAPGDVAVVLEGRPEFVGLWGLAKAGVVAALLNVNLRREPLAFCLGHSAAKALLYGGE	184				
QY	183	MASAEVHASLDPSLSLFCSSGSEWEPGAVPPSTEHLDPKADP-KHLPSCDPKGFDKL	241				
Db	185	MAAAVAEVSQGLSKLLKFCSDGLPESILPDQLDPLMLAEAPTTPLAQAPCKGMDRL	244				
QY	242	FYIYTSGLTKPAAVTVHSRYMAALVYVGFRRMPNDIVDCLPLIYSAGNIVGIGOC	301				
Db	245	FYIYTSGLTKPAAVTVHSRYMAALVYVGFRRMPNDIVDCLPLIYSAGNIVGIGOC	304				
QY	302	LLHGMTVWIRKKFSASFRWDDCIKYNCTIVQYIGELCRVLLNQPPEAEHQHVRMALGN	361				
Db	305	VYGLVWLRKKFSASFRWDDCIKYNCTIVQYIGELCRVLLNQPPEAEHQHVRMALGN	364				
QY	362	GLRQSTWTFNFSRPHTPQVAEYFQATECNCSGNFDSQVAGCFNSRLISFYPIRLVRV	421				
Db	365	GLRPAIWEETORFQVGFQGEFYGATECNCSIANMDKVGSCGFNSRLIHTVYPIRLVKV	424				

Db 430 RATGELERDKNGLVCPVCPGETGEMGVVKEIKEDILLKFBGYVSEGDATAKKIYDRVFKHGD 489
QY 483 QAYLTGDLVMDLGLYLFDRDTRFRWKGENVSTTEVEGLTSRLDMDADVAVGVVEVP 542
Db 490 KVFASGDILHWDGLYLFVDRDGTFRWKGENVSTTEVEGLIQPMVEDATVYGVTVG 549
QY 543 GTEGRAGMAVASPTGNCGLDERF---AQVLEKELPYARPIFLRLPELHKTGYKFKOK 598
Db 550 KMEGRAGMAGIVVKDGT-DVEKEIADITSRLTENLASIYALPIFIRUCKEVDRTGTFKLKK 608
QY 599 TELRKEGFDPAIVK-DPLFYLDQAQGRYVPLDQAYSRIOAG 639
Db 609 TDLQKQGLVACKGDPPIYWSAAKSYKPLTDKMQOODITG 650

RESULT 4
JW0107
very-long-chain acyl-CoA synthetase related protein - mouse
N:Alternate names: VIAGSR
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Sep-2000
C:Accession: JW0107
R:Berger, J.; Truppe, C.; Neumann, H.; Forss-Petter, S.
Biochem. Biophys. Res. Commun. 247, 255-260, 1998
A:Title: A novel relative of the very-long-chain acyl-CoA synthetase and fatty acid tran-
sferase from *Yersinia enterocolitica* serotype 4/O:3
A:Reference number: JW0107; MUID:98308102
A:Accession: JW0107
A:Molecule type: mRNA
A:Residues: 1-689

A:Cross-references: GB:AJ223959
A:Experimental source: liver
C:Comment: This protein likely functions as a plasma membrane transporter of long chain
cids.
C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase ho-
F:169-647/Domain: acetate--CoA ligase homology <ACL>

Query Match 28.8%; Score 974; DB 1; Length 689;
Best Local Similarity 37.2%; Pred. No. 1.5e-71;
Matches 251; Conservative 104; Mismatches 260; Indels 60; Gaps 18;

QY 1 MLGASLVGVLLSKVLKLPW-----TQVGFSLFLYL---GSGWRFIRVFTK 48
Db 43 VLLGLALLG-----RPWISSMHPWLSLVGAALTFLPLQPPPLRLHDKDAV 92
QY 49 IRRDIFGLVLLKVKAKVQCQLERTVPILFASVRRH---PDKALIFEGTD-TWHT 103
Db 93 TFKMLFYGL-----KFRRRLNKH--PPETFDALERQALWPRVALVCTGSGSSIT 143
QY 104 FROLDEYSSVANFLOARGLASG-----DVAEIFM--ENRNEFVGLMGLMAKLGVEAAL 155
Db 144 NSQLDARSQAAWLVKAK-LKDAVIONTRDAAAIIPLPSKITSALSVELGLAKLGPVAV 202
QY 156 INTNLRDALLHCLTTSRRARLVFGSEMAAICEVHAS-LDPSLSLFCSGSEWEPVAPPS 214
Db 203 INPHSGMFLHSHVRSAGASVLIQVDPDQENLEELVPLKLAENHCFYLGHSPP---TPG 259
QY 215 TEHLDPKLLKADPKHLPSCDPKGTOK-----LFYIVTSGTGLPKAAIVVHVSRYRMA-AL 269
Db 260 VEALGASLDAAPSD-PVPASLRATIKWKSFAIFTSGTGLPKALLSHERVIOVSNVL 318
QY 270 VYFGFRMRNDIVDCLPLIYHSGNIVIGQCLLHGMVTVIRKKSASRFNDDCIKYNCT 329
Db 319 SFCG--CRADDVVYVPLIYHIGLVFLGLQVGCATCVLAPKFSASRFAECRQHGVT 376
QY 330 IVQYIGELCRYLLNPPREAEHQVRAALGNGLQSIWTFNFSRFRHPIQVAEFYGAEC 389
Db 377 VILYGEILRYLCNWPQEPEDKIHVRLAMGNGLRANWKNFQRPGRPIRIWEFYGSTG 436
QY 390 NCSLGNFDSQVGCAGFNSRILSFVYPIRLVVRNEDTMELIRPDGVCIPCPGEGQLVG 449
Db 437 NVGLMNVYCHCGAVGTSILRLMIFPFVQFDIETAEPLRDKQFCIPVPEGKGLLIT 496

QY 450 RIIQKDPILRRDGYLNGQANNKKTAKDVFKKQDQAYITGDLVMDLGLYLFDRDGTGTF 509
Db 497 KVRKNQPPGLGRG--SQAESNRKLVANVRVGDLYFNTGDLVTLQDQEGFFVQDRLGDTF 554
QY 510 RWKGNVSTTEVEGLTSRLDMDADVAVGVVEVPCTEGRAGMAAV-ASPTGNCGLDERFAOV 568
Db 555 RWKGNVSTGEVESVLSLDFLEEVNVTGVVPGCEKGVGMAAVKLAPGKTFDQCKLYOH 614
QY 569 LEKELPYARPIFLRLPELHKTGYKFKTELRKEGFDPAIVKDPFLFYLDQAQGRYVPL 628
Db 615 VRSWLPAYATPHFIRIODSLEITNTYKLVKSLRVREGFDVGIADPLVILDNKAQTFRSL 674
QY 629 DOEAYSRIQAGEKL 643
Db 675 MPDVTQAVCEGTWKL 689

RESULT 5

H83284
probable very-long-chain acyl-CoA synthetase PA2893 [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H83284
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L-
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pa-
thogen
A:Reference number: A82950; MUID:20437337
A:Accession: H83284
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-608 <STO>
A:Cross-references: GB:AE004715; GB:AE004091; MID:99948977; PIDN:AAG06281.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2893
C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate--CoA ligase

Query Match 27.1%; Score 918.5; DB 2; Length 608;
Best Local Similarity 38.2%; Pred. No. 4.4e-67;
Matches 218; Conservative 86; Mismatches 229; Indels 37; Gaps 14;

QY 85 RHHPDKTALIFEGDTHWTFRQLDEYSSVANFLOARGLASGDVAAIFMENRNEFVCLWL 144
Db 53 RLYPDNFA-VLDG--QRRISTALFNGWANRLARAFKASGVGHGVSVAVMLENRVVELLAILA 110
QY 145 GMAKLGVEAALINTNLRDALLHCLTTSRRARLVFGSEMAAICEV-HASLDPSLSLFCFS 203
Db 111 ALAKLGAIGALVNTQGRKVLVHSLNLVKPGHFVVGEELEVEFVEHVLGNAGHCY-- 168
QY 204 GSW-----EPGAVPSPSTEHLDPILK-DAPKHLPCSPDKGTDKLFYIYTSGTGLPK 254
Db 169 --WYDDGDTLGDGSPGPMGRNMLRLAQGQTSNLEDTGRVRLKDSCFYIYTSGTGLPK 226
QY 255 AAIIVHVSRYR-MAALVYIGFRMPNDIVDCLPLIYHSGNIVIGQCLLHGMVTVIRKK 313
Db 227 ASIMSHGKWIKAYGFGHSGGLGORDVLYLTLCYHNNAVTVCSAALAGGAMALRRK 286
QY 314 FSASRFNDDCIKYNCTIVQYIGELCRYLLNPPREAEHQVRAALGNGLRQSIWTFNFS 373
Db 287 FSASGFKNDQVHYRATCFYIGELCRYLLNPPREAEHQVRAALGNGLRQSIWTFNFS 346
QY 374 RFHPIQVAEFYGAECN---CSLGNFDSQVGCAGFNSRILSFVYPIRLVVRNEDTMELIR 430
Db 347 RFEIQRITEFVASSEGNGITNFNFQNTV---GFSPTAFA-----IVRIDLNDPRVR 397
QY 431 GPDGVCIPCPGEGQLVGRILQIKDPLRRDGYLNGQANNKKTAKDVFKKQDQAYITGTV 490
Db 398 DAKGFMKVGKGVGLLILSISAKWP---PDGYTDPKASEAVILRDVFKKGDWAFNTGD- 453
QY 491 LVMDLGLYLF--FRDRTGDTFRWKGENVSTTEVEGLTSRLDMDADVAVGVVEPGTEGRA 548

RESULT 14

G70986
 probable coA ligase - Mycobacterium tuberculosis (strain H37Rv)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Aug-2000
 C:Accession: G70986
 C:Collector, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98293987
 A:Accession: G70986
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-532 <COL>
 A:Cross-references: GB:Z95890; GB:AL123456; NID:g3242245; PIDN:CAB09316.1; PID:g2131015
 A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: fadD1
 A:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology
 F:48-499/Domain: acetate--CoA ligase homology <ACL>

Query Match 10.6%; Score 358; DB 2; Length 532;
 Best Local Similarity 24.5%; Pred. No. 3.1e-21;
 Matches 145; Conservative 77; Mismatches 229; Indels 142; Gaps 20;

QY 82 STVRRHPDKTALIFEGTDHTWTFRLQDEYSSVANFQARGLASGDVAIAFENENRNFV 141
 Db 7 SLRQHVSDPTIAVKGGLQWTSQ-----YLAESARAALTIADPQRPTHIG 56
 QY 142 LWLG-----MAKI-----GVRAALINTLNRDAL-----LHC-----LTSRARALVFGS 181
 Db 57 SLGLNPEMLAALAAAGLVLCGLNTRRGDAADVRRADCCQIVVTVDADHRLDLGL 116
 QY 182 EMASACEVHASLDPSLSLFCSSGNEPAGVPPSTHLDPLLDKADPKHLPSCDKGFTKL 241
 Db 117 DLAGA-----RLDSTPRAELVAGDGAFFVRE-VDTM-----DPF 153
 QY 242 FYIYTGTTGLPKAAIVHVSRYRMAALVYIGFRMPNDIVDCLPLXHSAGNIGIGQC 301
 Db 154 MMFTSGTSGNKAIVPVSHLMATFAGRSUTERFGLTEQDTCVSMPLFHSNAVAGWAPA 213
 QY 302 LLHGMVTVIRKKSASFWDCCIKYNTIVQIGELCYLLNQPPREAHQHVRLMAGN 361
 Db 214 VVSG-AAIAPATFSATGFLDDVRRVHATYMYVGRPLAYILATPERDDADNPLRAFGN 272
 QY 362 GLRQSIWTFNSRFRHPIQVAEFGATE-----CN 390
 Db 273 EANDKIDIEFSRRFGV-QVEDFGSTENAVIVIRPPTGPGSIGRANGVAVNGETVTE 331
 QY 391 CSLGNFDSOVGACGNSRILSFYPIRLVRVNDTMMELIRGPDGVCIPCPGEPGOLVGR 450
 Db 332 CAVAREDAH-GAL-----TNAD-----EAIGE 352
 QY 451 IIOKDLPRFDGYLNO-GANNKKIAKDVFKGDQAYLITGDVLVMDLGYLFRDRTGTTF 509
 Db 353 LVNTTSGSGFTGYNDPEANEARHMGVYWSGLAY-----RDSEGWYLAGRTADWM 405
 QY 510 RWKGENVSTVEGTLRLDMDADVAVYGV--EVPGTGRAGMAVAVSPTGNC-D-LERFA 566
 Db 406 RVDGENLTAAPRIERILLYKAINRVAVYVDPYVGDQVMAALVLRAGDTFDPDAFEAL 465
 QY 567 QVLEKELPLYARPIFLRLPELHKGTGTYKFKQTELKKEG-----FDPAIVKDP 614
 Db 466 DA-QPDLSTKARPVIRIAADLPSTATKVLKRLQIDEGTAVGKADTLWVREP 517

RESULT 15

S40558
 probable carnitine--CoA ligase (EC 6.2.1.-) - Escherichia coli

C:Species: Escherichia coli
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C:Accession: E64724; S40558; I41013
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 .A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: E64724
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-522 <BLAT>
 A:Cross-references: GB:AE000114; GB:U00096; NID:g1786217; PIDN:AACT3148.1; PID:g17862
 A:Experimental source: strain K-12, substrain MG1655
 R:Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Miz
 submitted to the EMBL Data Library, December 1992
 A:Description: Systematic sequencing of the Escherichia coli genome: analysis of the
 A:Reference number: S40531
 A:Accession: S40558
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-522 <YUR>
 A:Cross-references: EMBL:D10483; NID:g216434; PIDN:BAA01313.1; PID:g216462
 R:Eichler, K.; Bourgis, F.; Buchet, A.; Kleber, H.P.; Mandrand-Berthelot, M.A.
 Mol. Microbiol. 13, 775-786, 1994
 A:Title: Molecular characterization of the cai operon necessary for carnitine metabol
 A:Reference number: I41010; MUID:95115548
 A:Accession: I41013
 A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-102, 'R', 104-256, 'PR', 259-290, 'R', 292-332, 'S', 334-349, 'A', 351-378, 'V', 38
 A:Cross-references: EMBL:X73904; NID:g563860; PIDN:CAA52113.1; PID:g563864
 A:Experimental source: strain O44 K74
 C:Genetics:
 A:Gene: caiC
 C:Function:
 A:Pathway: lysine degradation; tryptophan metabolism
 C:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology
 C:Keywords: acid-thiol ligase; ATP; phosphoprotein; transmembrane protein
 F:63-521/Domain: acetate--CoA ligase homology <ACL>
 F:81-97/Domain: transmembrane #status predicted <TM1>
 F:235-251/Domain: transmembrane #status predicted <TM2>
 F:194/Active site: Lys #status predicted

Query Match 10.4%; Score 350.5; DB 2; Length 522;
 Best Local Similarity 24.1%; Pred. No. 1.2e-20;
 Matches 137; Conservative 86; Mismatches 275; Indels 71; Gaps 18;

QY 52 DIFGGLVLLKAKVRQCLQERTVPIPLFASVRRHPDKTALIFE---GTDHTWTFRLD 108
 Db 7 DIIGG-----QHLRQMWDDLDV-----YGHKTALICESGGVYVNRYSYLELN 49
 QY 109 EYSSVANFQARGLASGDVAIAFENENRNFVGLWLGMAKIGVEAALINTLNRDALLHC 168
 Db 50 QEINTNANLTYTIGIRKGDVKAHLHLDNCPFEICFWGLAKIGAINVPIVARLLCESAWI 109
 QY 169 LTTSRARALVFGSEMAAICEVHASLDPSLSLFCSSGNEPAGV--PSTHLDPLLDKAP 226
 Db 110 LONSQACLLVTSQAQFPMYQIQOEDATQLRHIC---LTDVALPADDDGVSSFTQLKNQOP 166
 QY 227 KHLPSCKDKGFTDKLYIYTGTTGLPKAAIVHVSRYRMAALVYIG---FMRPNDIYV 283
 Db 167 ATLCAPIPLSTDTAEILFTSGTTSRPGVWITP---YNLRFAGYYSWAQCALRDDVYL 223
 QY 284 DCLPLXHSAGNIGVIGQCLLHGMVTVIRKKSASREWDCCIKYNTIVQIGELCYLLN 343
 Db 224 TVMPAFHIDCQCTAANAAPASAGATFVLVKEYSARAFWGQVQYRATVETCPIMPTLAV 283
 QY 344 QPPREAHQHVRLMAGN-GLRQSIWTFNSRFRHPIQVAEFGATECNCS-LGNFDS--- 398
 Db 284 QPPSANDQQHRLREVLYNLNLSQEKDAFCERFGV-RLITSYGMTETIVGIIGDRPGDKR 342

QY 399 ---QVACGFSRITLSPVYPIRLVRVNEDTMELIRGPDG-VCIPCOGPGQVLVGRIOK 454
 Db 343 RWFSGRVGF-----CYEAER---DDHNRPLPAGEIGEICI---KGIPGKTIFK----- 386
 QY 455 DPLRRFDGYLNOGANNKKIAKDVFKKGDQAYL-TGDVLMDELGYLYFRDRTGDTFRWKG 513
 Db 387 -----EYFLNPQATAKVLEAD-----GWLHTGDTGYRDEDEFFVVDRCNMIKRG 433
 QY 514 ENVSTTEVEGTLSRLLDMAVDVYGVVPGTEGRAGMAAVASPTGNCDLERFAQVLEKEL 573
 Db 434 ENVSCVELENIIAHPKIQIDIVVVGIKDSIRDEAIAKAFVVLNEGTELSEEEFFRCEQNM 493
 QY 574 PLYARPIFLRLPELHKGTGYKFKOTELR 602
 Db 494 AKFVPSYLEIRKDLPRNCCKIIRNLK 522

Search completed: July 16, 2001, 18:13:56
 Job time: 157 sec

7